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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/464,685

DATE: 08/25/2000
TIME: 12:55:07

Input Set : A:\464685.txt
Output Set : N:\CRF3\08252000\I464685.raw

5 <110> APPLICANT: Glucksmann, Maria A.
7 Hodge, Martin G.
11 <120> TITLE OF INVENTION: 2871 RECEPTOR, A NOVEL G-PROTEIN COUPLED RECEPTOR
15 <130> FILE REFERENCE: 5800-2A (035800/183295)
19 <140> CURRENT APPLICATION NUMBER: US 09/464,685
21 <141> CURRENT FILING DATE: 1999-12-16
23 <150> PRIOR APPLICATION NUMBER: US 09/324,465
24 <151> PRIOR FILING DATE: 1999-06-02
27 <150> PRIOR APPLICATION NUMBER: 09/088,857
29 <151> PRIOR FILING DATE: 1998-06-02
33 <160> NUMBER OF SEQ ID NOS: 6
37 <170> SOFTWARE: PatentIn Ver. 2.0.
41 <210> SEQ ID NO: 1
43 <211> LENGTH: 358
45 <212> TYPE: PRT
47 <213> ORGANISM: Homo sapiens
51 <400> SEQUENCE: 1
53 Met Gly Phe Asn Leu Thr Leu Ala Lys Leu Pro Asn Asn Glu Leu His
55 1 5 10 15
59 Gly Gln Glu Ser His Asn Ser Gly Asn Arg Ser Asp Gly Pro Gly Lys
61 20 25 30
65 Asn Thr Thr Leu His Asn Glu Phe Asp Thr Ile Val Leu Pro Val Leu
67 35 40 45
71 Tyr Leu Ile Ile Phe Val Ala Ser Ile Leu Leu Asn Gly Leu Ala Val
73 50 55 60
77 Trp Ile Phe Phe His Ile Arg Asn Lys Thr Ser Phe Ile Phe Tyr Leu
79 65 70 75 80
83 Lys Asn Ile Val Val Ala Asp Leu Ile Met Thr Leu Thr Phe Pro Phe
85 85 90 95
89 Arg Ile Val His Asp Ala Gly Phe Gly Pro Trp Tyr Phe Lys Phe Ile
91 100 105 110
95 Leu Cys Arg Tyr Thr Ser Val Leu Phe Tyr Ala Asn Met Tyr Thr Ser
97 115 120 125
101 Ile Val Phe Leu Gly Leu Ile Ser Ile Asp Arg Tyr Leu Lys Val Val
103 130 135 140
107 Lys Pro Phe Gly Asp Ser Arg Met Tyr Ser Ile Thr Phe Thr Lys Val
109 145 150 155 160
113 Leu Ser Val Cys Val Trp Val Ile Met Ala Val Leu Ser Leu Pro Asn
115 165 170 175
119 Ile Ile Leu Thr Asn Gly Gln Pro Thr Glu Asp Asn Ile His Asp Cys
121 180 185 190
125 Ser Lys Leu Lys Ser Pro Leu Gly Val Lys Trp His Thr Ala Val Thr
127 195 200 205
131 Tyr Val Asn Ser Cys Leu Phe Val Ala Val Leu Val Ile Leu Ile Gly
133 210 215 220
137 Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His Lys Ser Ser Arg Gln Phe
139 225 230 235 240

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143 Ile Ser Gln Ser Ser Arg Lys Arg Lys His Asn Gln Ser Ile Arg Val
145           245           250           255
149 Val Val Ala Val Phe Phe Thr Cys Phe Leu Pro Tyr His Leu Cys Arg
151           260           265           270
155 Ile Pro Phe Thr Phe Ser His Leu Asp Arg Leu Leu Asp Glu Ser Ala
157           275           280           285
161 Gln Lys Ile Leu Tyr Tyr Cys Lys Glu Ile Thr Leu Phe Leu Ser Ala
163           290           295           300
167 Cys Asn Val Cys Leu Asp Pro Ile Ile Tyr Phe Phe Met Cys Arg Ser
169 305           310           315           320
173 Phe Ser Arg Arg Leu Phe Lys Lys Ser Asn Ile Arg Thr Arg Ser Glu
175           325           330           335
179 Ser Ile Arg Ser Leu Gln Ser Val Arg Arg Ser Glu Val Arg Ile Tyr
181           340           345           350
185 Tyr Asp Tyr Thr Asp Val
187           355
192 <210> SEQ ID NO: 2
194 <211> LENGTH: 1489
196 <212> TYPE: DNA
198 <213> ORGANISM: Homo sapiens
202 <400> SEQUENCE: 2
204 ccacgcgtcc ggagaatttg aaaggggtgcc ccaaaggaca atctctaaag gggtaaggga 60
206 gataacctacc ttgtctggta ggggagatgt ttctgtttca tgctttacca gaaaatccac 120
208 ttccctgcgcg accttagttt caaagcttat tcttaattag agacaagaaa cctgtttcaa 180
210 cttgaagaca ccgtatgagg tgaatggaca gccagccacc acaatgaaag aaatcaaacc 240
212 aggaataaacc tatgctgaac ccacgcctca atcgtcccca agtgtttcct gacacgcac 300
214 ttgtcttaca gtgcatcaca actgaagaat ggggttcaac ttgacgcttg caaaattacc 360
216 aaataacgag ctgcacggcc aagagagtea caattcaggc aacaggagcg acgggccagg 420
218 aaagaacacc acccttcaca atgaatttga cacaattgtc ttgcccgtgc tttatctcat 480
220 tatatttgty gcaagcatct tgctgaatgg tttagcagtg tggatcttct tccacattag 540
222 gaataaaacc agcttcatat tctatctcaa aaacatagtg gttgcagacc tcataatgac 600
224 gctgacattt ccatttcgaa tagtccatga tgcaggattt ggaccttggt acttcaaagt 660
226 tattctctgc agatacactt cagttttgtt ttatgcaaac atgtatactt ccacgtgtt 720
228 ccttgggctg ataagcattg atcgtatctt gaaggtggtc aagccatttg gggactctcg 780
230 gatgtacagc ataaccttca cgaagggttt atctgtttgt gtttgggtga tcatggctgt 840
232 ttgtcttttg ccaaaccatc tcttgacaaa tggtcagcca acagaggaca atatccatga 900
234 ctgctcaaaa cttaaaagtc ctttgggggt caaatggcat acggcagtea cctatgtgaa 960
236 cagctgcttg tttgtggcgc tgctgggtgat tctgatcgga tgttacatag ccatatccag 1020
238 gtacatccac aaatccagca ggcaattcat aagtcagtea agccgaaagc gaaaacataa 1080
240 ccagagcacc agggttgttg tggctgtgtt ttttacctgc tttctacat atcacttggt 1140
242 cagaattcct tttactttta gtcacttaga caggctttta gatgaatctg cacaataaat 1200
244 cctataattac tgcaaaagaaa ttacactttt cttgtctgcg tgtaatgttt gcctggatcc 1260
246 aataattttac tttttcatgt gtaggtcatt ttcaagaagg ctgttcaaaa aatcaaatat 1320
248 cagaaccagg agtgaaagca tcagatcact gcaaagtgtg agaagatcgg aagttcgcac 1380
250 atattatgat tacactgatg ttagggcctt ttattgtttg ttggaatcga tatgtacaaa 1440
252 gtgtaataaa atgtttcttt tcattaataa aamaaaaaaa aaaaaaaag 1489
255 <210> SEQ ID NO: 3
257 <211> LENGTH: 269
259 <212> TYPE: PRT

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261 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
267 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus
269     sequence of the seven transmembrane domain
271     rhodopsin superfamily from the Prosite data base
275 <400> SEQUENCE: 3
277 Gly Asn Ile Leu Val Ile Trp Val Ile Cys Arg Tyr Arg Arg Met Arg
279   1           5           10           15
283 Thr Pro Met Asn Tyr Phe Ile Val Asn Leu Ala Val Ala Asp Leu Leu
285           20           25           30
289 Phe Ser Leu Phe Thr Met Pro Phe Trp Met Val Tyr Tyr Val Met Gln
291           35           40           45
295 Gly Arg Trp Trp Pro Phe Gly Asp Phe Met Cys Arg Ile Trp Met Tyr Phe
297           50           55           60
301 Asp Tyr Met Asn Met Tyr Ala Ser Ile Phe Phe Leu Thr Cys Ile Ser
303           65           70           75           80
307 Ile Asp Arg Tyr Leu Trp Ala Ile Cys His Pro Met Arg Tyr Met Arg
309           85           90           95
313 Trp Met Thr Pro Arg His Arg Ala Trp Val Met Ile Ile Ile Trp
315           100          105          110
319 Val Met Ser Phe Leu Ile Ser Met Pro Pro Phe Leu Met Phe Arg Trp
321           115          120          125
325 Ser Thr Tyr Arg Asp Glu Asn Glu Trp Asn Met Thr Trp Cys Met Ile
327           130          135          140
331 Tyr Asp Trp Pro Glu Trp Met Trp Arg Trp Tyr Val Ile Leu Met Thr
333           145          150          155          160
337 Ile Ile Met Gly Phe Tyr Ile Pro Met Ile Ile Met Leu Phe Cys Tyr
339           165          170          175
343 Trp Arg Ile Tyr Arg Ile Ala Arg Leu Trp Met Arg Met Ile Pro Ser
345           180          185          190
349 Trp Gln Arg Arg Arg Arg Met Ser Met Arg Arg Glu Arg Arg Ile Val
351           195          200          205
355 Lys Met Leu Ile Ile Ile Met Val Val Phe Ile Ile Cys Trp Leu Pro
357           210          215          220
361 Tyr Phe Ile Val Met Phe Met Asp Thr Leu Met Met Trp Trp Phe Cys
363           225          230          235          240
367 Glu Phe Cys Ile Trp Arg Arg Leu Trp Met Tyr Ile Phe Glu Trp Leu
369           245          250          255
373 Ala Tyr Val Asn Cys Pro Cys Ile Asn Pro Ile Ile Tyr
375           260          265
382 <210> SEQ ID NO: 4
384 <211> LENGTH: 20
386 <212> TYPE: DNA
388 <213> ORGANISM: Artificial Sequence
392 <220> FEATURE:
394 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
396     oligonucleotide primer
400 <400> SEQUENCE: 4
402 atcggtgttcc ttgggctgat

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407 <210> SEQ ID NO: 5
409 <211> LENGTH: 19
411 <212> TYPE: DNA
413 <213> ORGANISM: Artificial Sequence
417 <220> FEATURE:
419 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
421 oligonucleotide primer
425 <400> SEQUENCE: 5
427 tccgagagtc cccaaatgg 19
432 <210> SEQ ID NO: 6
434 <211> LENGTH: 29
436 <212> TYPE: DNA
438 <213> ORGANISM: Artificial Sequence
442 <220> FEATURE:
444 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
446 oligonucleotide probe
450 <400> SEQUENCE: 6
452 agcattgata gctatctgaa ggtggtcaa 29

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/464,685

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